

THAT WHICH IS CLAIMED:

1. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

5 (a) a polypeptide sequence comprising the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 37;

10 (b) a polypeptide having at least 80% sequence identity with at least one of the sequences of (a), wherein said polypeptide retains peroxidase-like activity;

(c) a polypeptide encoded by a nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, and 36; and

15 (d) a fragment comprising at least 20 contiguous amino acids of at least one of the amino acid sequences set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 37, wherein said fragment has peroxidase-like activity.

20 2. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence set forth in SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 36;

25 (b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 37;

(c) a nucleotide sequence comprising at least 16 contiguous nucleotides of a nucleotide sequence of (a) or (b), wherein said sequence encodes a polypeptide having peroxidase-like activity;

30 (d) a nucleotide sequence having at least 60% sequence identity with at least one nucleotide sequence of (a) or (b), wherein said nucleotide sequence

having at least 60% sequence identity with at least one nucleotide sequence of (a) or (b) encodes a polypeptide having peroxidase-like activity;

(e) a nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence of (a) or (b), wherein said nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence of (a) or (b) encodes a polypeptide having peroxidase-like activity; and

(f) a nucleotide sequence complementary to a nucleotide sequence of (a), (b), (c), (d), or (e).

3. The nucleic acid molecule of claim 2, wherein said nucleotide sequence is operably linked to a promoter that drives expression in a plant cell.

4. An expression vector comprising the nucleic acid molecule of claim 3.

5. A host cell having stably incorporated into its genome at least one nucleotide sequence, wherein said nucleotide sequence is operably linked to a heterologous promoter that drives expression in the host cell, wherein said nucleotide sequence is selected from the group consisting of:

(a) the nucleotide sequence set forth in SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 36;

(b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 37;

(c) a nucleotide sequence comprising at least 16 contiguous nucleotides of a nucleotide sequence of (a) or (b), wherein said sequence encodes a polypeptide having peroxidase-like activity;

(d) a nucleotide sequence having at least 60% sequence identity with at least one nucleotide sequence of (a) or (b), wherein said nucleotide sequence having at least 60% sequence identity with at least one nucleotide sequence of (a) or (b) encodes a polypeptide having peroxidase-like activity;

(e) a nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence of (a) or (b), wherein said nucleotide sequence

that hybridizes under stringent conditions to at least one nucleotide sequence of (a) or (b) encodes a polypeptide having peroxidase-like activity; and
(f) a nucleotide sequence complementary to a nucleotide sequence of (a), (b), (c), (d), or (e).

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6. The host cell of claim 5, wherein said cell is a plant cell.

7. A plant having stably incorporated into its genome at least one nucleotide sequence operably linked to a heterologous promoter that drives expression in a plant cell, wherein said nucleotide sequence is selected from the group consisting of:

- 10 (a) the nucleotide sequence set forth in SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 36;
- (b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 37;
- 15 (c) a nucleotide sequence comprising at least 16 contiguous nucleotides of a nucleotide sequence of (a) or (b), wherein said sequence encodes a polypeptide having peroxidase-like activity;
- (d) a nucleotide sequence having at least 60% sequence identity with at least one nucleotide sequence of (a) or (b), wherein said nucleotide sequence
- 20 having at least 60% sequence identity with at least one nucleotide sequence of (a) or (b) encodes a polypeptide having peroxidase-like activity;
- (e) a nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence of (a) or (b), wherein said nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence of
- 25 (a) or (b) encodes a polypeptide having peroxidase-like activity; and
- (f) a nucleotide sequence complementary to a nucleotide sequence of (a), (b), (c), (d), or (e).

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8. The plant of claim 7, wherein said promoter is a constitutive promoter.

9. The plant of claim 7, wherein said promoter is a tissue-preferred promoter.

10. The plant of claim 7, wherein said promoter is an inducible promoter.
11. The plant of claim 10, wherein said promoter is a pathogen-inducible
5 promoter.
12. The plant of claim 7, wherein said plant is a monocot.
13. The plant of claim 12, wherein said monocot is maize, rice, or wheat.
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14. The plant of claim 12, wherein said monocot is maize.
15. The plant of claim 7, wherein said plant is a dicot.
16. The plant of claim 15, wherein said dicot is soybean or sunflower.
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17. The transformed seed of the plant of claim 7.
18. A method for enhancing the defense response in a plant, said method
20 comprising stably incorporating into the genome of said plant at least one nucleotide
sequence operably linked to a heterologous promoter that drives expression in a plant
cell, wherein said nucleotide sequence is selected from the group consisting of:
- (a) the nucleotide sequence set forth in SEQ ID NO:3, 7, 9, 20, 30, or
32;
 - 25 (b) a nucleotide sequence encoding the amino acid sequence set forth
in SEQ ID NO:4, 8, 10, 21, 31, or 33;
 - (c) a nucleotide sequence comprising at least 16 contiguous
nucleotides of a nucleotide sequence of (a) or (b), wherein said sequence encodes
a polypeptide having peroxidase-like activity;
 - 30 (d) a nucleotide sequence having at least 60% sequence identity with
at least one nucleotide sequence of (a) or (b), wherein said nucleotide sequence

having at least 60% sequence identity with at least one nucleotide sequence of (a) or (b) encodes a polypeptide having peroxidase-like activity;

(e) a nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence of (a) or (b), wherein said nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence of (a) or (b) encodes a polypeptide having peroxidase-like activity; and

(f) a nucleotide sequence complementary to a nucleotide sequence of (a), (b), (c), (d), or (e).

10 19. The method of claim 18, wherein said promoter is a constitutive promoter.

20. The method of claim 18, wherein said promoter is a pathogen inducible promoter.

15 21. The method of claim 18, wherein said plant is a monocot.

22. The method of claim 21, wherein said monocot is maize, wheat, or rice.

23. The method of claim 18, wherein said plant is a dicot.

20 24. The method of claim 23, wherein said dicot is soybean or sunflower.

25 25. A method for enhancing the defense response in a plant, said method comprising stably incorporating into the genome of said plant at least one nucleotide sequence operably linked to a heterologous promoter that drives expression in a plant cell, wherein said defense response does not include a response to an insect, and wherein said nucleotide sequence is selected from the group consisting of:

(a) the nucleotide sequence set forth in SEQ ID NO:1, 5, 11, 13, 16, 18, 20, 22, 24, 26, 34, or 36;

30 (b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO:2, 6, 12, 14, 17, 19, 23, 25, 27, 29, 35, or 37;

(c) a nucleotide sequence comprising at least 16 contiguous nucleotides of a nucleotide sequence of (a) or (b), wherein said sequence encodes a polypeptide having peroxidase-like activity;

5 (d) a nucleotide sequence having at least 60% sequence identity with at least one nucleotide sequence of (a) or (b), wherein said nucleotide sequence having at least 60% sequence identity with at least one nucleotide sequence of (a) or (b) encodes a polypeptide having peroxidase-like activity;

10 (e) a nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence of (a) or (b), wherein said nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence of (a) or (b) encodes a polypeptide having peroxidase-like activity; and

(f) a nucleotide sequence complementary to a nucleotide sequence of (a), (b), (c), (d), or (e).

15 26. The method of claim 25, wherein said promoter is a constitutive promoter.

27. The method of claim 25, wherein said promoter is a pathogen inducible promoter.

20 28. The method of claim 25, wherein said plant is a monocot.

29. The method of claim 28, wherein said monocot is maize, wheat, or rice.

30. The method of claim 25 wherein said plant is a dicot.

25 31. The method of claim 30, wherein said dicot is soybean or sunflower.

32. A method for enhancing stalk strength in a plant, said method comprising stably incorporating into the genome of said plant at least one nucleotide sequence operably linked to a heterologous promoter that drives expression in a plant cell, wherein said nucleotide sequence is selected from the group consisting of:

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(a) the nucleotide sequence set forth in SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 36;

(b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 37;

5 (c) a nucleotide sequence comprising at least 16 contiguous nucleotides of a nucleotide sequence of (a) or (b), wherein said sequence encodes a polypeptide having peroxidase-like activity;

(d) a nucleotide sequence having at least 60% sequence identity with at least one nucleotide sequence of (a) or (b), wherein said nucleotide sequence having at least 60% sequence identity with at least one nucleotide sequence of (a) or (b) encodes a polypeptide having peroxidase-like activity;

(e) a nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence of (a) or (b), wherein said nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence of (a) or (b) encodes a polypeptide having peroxidase-like activity; and

(f) a nucleotide sequence complementary to a nucleotide sequence of (a), (b), (c), (d), or (e).

33. The method of claim 32, wherein said promoter is a constitutive promoter.

20 34. The method of claim 32, wherein said promoter is a pathogen inducible promoter.

35. The method of claim 32, wherein said plant is a monocot.

25 36. The plant of claim 35, wherein said monocot is maize, wheat, or rice.

37. The method of claim 32, wherein said plant is a dicot.

30 38. The method of claim 37, wherein said dicot is soybean or sunflower.

39. A method for preventing oxidative damage following anoxia in a plant, said method comprising stably incorporating into the genome of said plant at least one nucleotide sequence operably linked to a heterologous promoter that drives expression in a plant cell, wherein said nucleotide sequence is selected from the group consisting of:

- 5 (a) the nucleotide sequence set forth in SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 36;
- (b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 37;
- (c) a nucleotide sequence comprising at least 16 contiguous
10 nucleotides of a nucleotide sequence of (a) or (b), wherein said sequence encodes a polypeptide having peroxidase-like activity;
- (d) a nucleotide sequence having at least 60% sequence identity with at least one nucleotide sequence of (a) or (b), wherein said nucleotide sequence having at least 60% sequence identity with at least one nucleotide sequence of (a)
15 or (b) encodes a polypeptide having peroxidase-like activity;
- (e) a nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence of (a) or (b), wherein said nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence of (a) or (b) encodes a polypeptide having peroxidase-like activity; and
- 20 (f) a nucleotide sequence complementary to a nucleotide sequence of (a), (b), (c), (d), or (e).

40. A method of breeding resistance to viral, bacterial, or fungal pathogens into plants, said method comprising:

- 25 (a) selecting at least one nontransgenic plant that constitutively expresses a nucleic acid molecule comprising a nucleotide sequence encoding an amino acid selected from the group consisting of the amino acid sequences set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37; wherein said nontransgenic plant expresses said nucleic acid molecule in
30 the absence of pathogen or chemical induction;
- (b) using said nontransgenic plant in a breeding program; and

(c) selecting pathogen resistant progeny with desired phenotypic traits.

41. The method of claim 40, wherein said nontransgenic plant is maize.

5 42. A method of selecting, from a population of plants, plants that are resistant to viral, bacterial, or fungal pathogens and that constitutively express a nucleic acid molecule comprising a nucleotide sequence encoding an amino acid selected from the group consisting of the amino acid sequences set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37, said method comprising:

- 10 (a) detecting the expression of said nucleic acid molecule, or evaluating the resistance to viral, bacterial, or fungal pathogens; and
- (b) selecting plants that are resistant to viral, bacterial, or fungal pathogens.

15 43. The method of claim 42, wherein said plants are maize.